$S V$

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _09/937,187_

Source: _PCT/09_

Date Processed by STIC: _2/6/2002_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
   http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission
   User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
   Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
           Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
   2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
   Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/937,187

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length

Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences
(OLD RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)　　SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences
(NEW RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10 ____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)　(Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

PCT/09

RAW SEQUENCE LISTING   DATE: 02/06/2002
PATENT APPLICATION: US/09/937,187   TIME: 18:41:31

Input Set : A:\Neb-164.app
Output Set: N:\CRF3\02062002\I937187.raw

PR 1-5

Does Not Comply
Corrected Diskette Needed

```
 3 <110> APPLICANT: SANDMAN, KAREN E.
 4        NOREN, CHRISTOPHER J.
 5        NEW ENGLAND BIOLABS, INC.
 7 <120> TITLE OF INVENTION: SURFACE DISPLAY OF SELENOCYSTEINE-CONTAINING PEPTIDES
 9 <130> FILE REFERENCE: NEB-164-PCT
11 <140> CURRENT APPLICATION NUMBER: US/09/937,187
12 <141> CURRENT FILING DATE: 2002-01-08
14 <150> PRIOR APPLICATION NUMBER: 60/134,286
15 <151> PRIOR FILING DATE: 1999-05-14
17 <160> NUMBER OF SEQ ID NOS: 42
19 <170> SOFTWARE: PatentIn Ver. 2.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 38
23 <212> TYPE: RNA
24 <213> ORGANISM: Synthetic
26 <220> FEATURE:
27 <223> OTHER INFORMATION: N = A, G, C, or U
29 <220> FEATURE:
30 <223> OTHER INFORMATION: K = G and U
32 <400> SEQUENCE: 1
33 nnknnknnkn nkugannknn knnkucggcc gaaacaug                        38
35 <210> SEQ ID NO: 2
36 <211> LENGTH: 24
37 <212> TYPE: DNA
38 <213> ORGANISM: Synthetic
40 <400> SEQUENCE: 2
41 tcgtcttttc cttgaaagtc gcct                                       24
43 <210> SEQ ID NO: 3
44 <211> LENGTH: 24
45 <212> TYPE: DNA
46 <213> ORGANISM: Synthetic
48 <400> SEQUENCE: 3
49 aagtgtacgc tttgatctat gctg                                       24
51 <210> SEQ ID NO: 4
52 <211> LENGTH: 24
53 <212> TYPE: DNA
54 <213> ORGANISM: Synthetic
56 <400> SEQUENCE: 4
57 ttgcttttgc cttgaaatgt tctt                                       24
59 <210> SEQ ID NO: 5
60 <211> LENGTH: 24
61 <212> TYPE: DNA
62 <213> ORGANISM: Synthetic
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see item 10 on Error Summary Sheet

item 10

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/937,187

DATE: 02/06/2002
TIME: 18:41:31

Input Set : A:\Neb-164.app
Output Set: N:\CRF3\02062002\I937187.raw

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 64 <400> SEQUENCE: 5
 65 atgactacgc agtgaccttc tctg                                    24
 67 <210> SEQ ID NO: 6
 68 <211> LENGTH: 24
 69 <212> TYPE: DNA
 70 <213> ORGANISM: Synthetic
 72 <400> SEQUENCE: 6
 73 catattccgc cgtgaacgaa tcct                                    24
 75 <210> SEQ ID NO: 7
 76 <211> LENGTH: 24
 77 <212> TYPE: DNA
 78 <213> ORGANISM: Synthetic
 80 <400> SEQUENCE: 7
 81 aaggctctgt gttgacagga ttcg                                    24
 83 <210> SEQ ID NO: 8
 84 <211> LENGTH: 24
 85 <212> TYPE: DNA
 86 <213> ORGANISM: Synthetic
 88 <400> SEQUENCE: 8
 89 cttcttccgt gttgagctca gccg                                    24
 91 <210> SEQ ID NO: 9
 92 <211> LENGTH: 24
 93 <212> TYPE: DNA
 94 <213> ORGANISM: Synthetic
 96 <400> SEQUENCE: 9
 97 catcatccga cttgagctaa gcag                                    24
 99 <210> SEQ ID NO: 10
100 <211> LENGTH: 24
101 <212> TYPE: DNA
102 <213> ORGANISM: Synthetic
104 <400> SEQUENCE: 10
105 atgcctccta cgtgaatggc tacg                                    24
107 <210> SEQ ID NO: 11
108 <211> LENGTH: 24
109 <212> TYPE: DNA
110 <213> ORGANISM: Synthetic
112 <400> SEQUENCE: 11
113 aattggtttt cttgactgac tacg                                    24
115 <210> SEQ ID NO: 12
116 <211> LENGTH: 24
117 <212> TYPE: DNA
118 <213> ORGANISM: Synthetic
120 <400> SEQUENCE: 12
121 ctgcatccga cgtgagctcg gcct                                    24
123 <210> SEQ ID NO: 13
124 <211> LENGTH: 24
125 <212> TYPE: DNA
126 <213> ORGANISM: Synthetic
128 <400> SEQUENCE: 13
```

```
129 gatagggggc cttgagcgaa gatt                                    24
131 <210> SEQ ID NO: 14
132 <211> LENGTH: 24
133 <212> TYPE: DNA
134 <213> ORGANISM: Synthetic
136 <400> SEQUENCE: 14
137 gcgtctttgc cttgaaggac gagt                                    24
139 <210> SEQ ID NO: 15
140 <211> LENGTH: 24
141 <212> TYPE: DNA
142 <213> ORGANISM: Synthetic
144 <400> SEQUENCE: 15
145 ttgccgcgtc agtgatggtc tccg                                    24
147 <210> SEQ ID NO: 16
148 <211> LENGTH: 24
149 <212> TYPE: DNA
150 <213> ORGANISM: Synthetic
152 <400> SEQUENCE: 16
153 ttgactggta cgtgatgtca gaat                                    24
155 <210> SEQ ID NO: 17
156 <211> LENGTH: 24
157 <212> TYPE: DNA
158 <213> ORGANISM: Synthetic
160 <400> SEQUENCE: 17
161 gaggcgtcgc gttgatgttc gact                                    24
163 <210> SEQ ID NO: 18
164 <211> LENGTH: 24
165 <212> TYPE: DNA
166 <213> ORGANISM: Synthetic
168 <400> SEQUENCE: 18
169 aagttggctc gttgatcggc gtcg                                    24
171 <210> SEQ ID NO: 19
172 <211> LENGTH: 24
173 <212> TYPE: DNA
174 <213> ORGANISM: Synthetic
176 <400> SEQUENCE: 19
177 aatggggcgc agtgatcgag gcat                                    24
179 <210> SEQ ID NO: 20
180 <211> LENGTH: 24
181 <212> TYPE: DNA
182 <213> ORGANISM: Synthetic
184 <400> SEQUENCE: 20
185 gcgagtccta cttgatttaa gccg                                    24
187 <210> SEQ ID NO: 21
188 <211> LENGTH: 24
189 <212> TYPE: DNA
190 <213> ORGANISM: Synthetic
192 <400> SEQUENCE: 21
193 tgtgctcatc cgtgatctac tcgt                                    24
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/937,187

DATE: 02/06/2002
TIME: 18:41:31

Input Set : A:\Neb-164.app
Output Set: N:\CRF3\02062002\I937187.raw

```
195 <210> SEQ ID NO: 22
196 <211> LENGTH: 24
197 <212> TYPE: DNA
198 <213> ORGANISM: Synthetic
200 <400> SEQUENCE: 22
201 cagtcgacgc ggtgatggaa tgat                                          24
203 <210> SEQ ID NO: 23
204 <211> LENGTH: 24
205 <212> TYPE: DNA
206 <213> ORGANISM: Synthetic
208 <400> SEQUENCE: 23
209 attgtggagt cgtgattgaa tccg                                          24
211 <210> SEQ ID NO: 24
212 <211> LENGTH: 24
213 <212> TYPE: DNA
214 <213> ORGANISM: Synthetic
216 <400> SEQUENCE: 24
217 acgcagcgta tgtgattgcc gccc                                          24
219 <210> SEQ ID NO: 25
220 <211> LENGTH: 24
221 <212> TYPE: DNA
222 <213> ORGANISM: Synthetic
224 <400> SEQUENCE: 25
225 gtgcagtata cgtgattgcc gaag                                          24
227 <210> SEQ ID NO: 26
228 <211> LENGTH: 24
229 <212> TYPE: DNA
230 <213> ORGANISM: Synthetic
232 <400> SEQUENCE: 26
233 gctgggcagt cgtgatcgac tgat                                          24
235 <210> SEQ ID NO: 27
236 <211> LENGTH: 24
237 <212> TYPE: DNA
238 <213> ORGANISM: Synthetic
240 <400> SEQUENCE: 27
241 ctgtctgcga gtcgatcgca gttt                                          24
243 <210> SEQ ID NO: 28
244 <211> LENGTH: 8
245 <212> TYPE: PRT
246 <213> ORGANISM: Synthetic
248 <220> FEATURE:
249 <223> OTHER INFORMATION: At position 5, X = Selenocysteine
251 <400> SEQUENCE: 28
252 Ser Ala Arg Val Xaa His Gly Pro
253   1              5
256 <210> SEQ ID NO: 29
257 <211> LENGTH: 98
258 <212> TYPE: DNA
259 <213> ORGANISM: Synthetic
```

```
261  <400> SEQUENCE: 29
262  catgtttcgg ccgtaccgac cgattggtgc agacctgcaa ccgatgggcc gtgtcagaca 60
263  cgagcgctag agtgagaata gaaaggtacc cgggcatg                         98
265  <210> SEQ ID NO: 30
266  <211> LENGTH: 25
267  <212> TYPE: DNA
268  <213> ORGANISM: Synthetic
270  <400> SEQUENCE: 30
271  catgcccggg tacctttcta ttctc                                       25
273  <210> SEQ ID NO: 31
274  <211> LENGTH: 20
275  <212> TYPE: DNA
276  <213> ORGANISM: Synthetic
278  <400> SEQUENCE: 31
279  ccctcatagt tagcgtaacg                                             20
281  <210> SEQ ID NO: 32
282  <211> LENGTH: 10
283  <212> TYPE: PRT
284  <213> ORGANISM: Synthetic
286  <220> FEATURE:
287  <223> OTHER INFORMATION: At position 5, X = Selenocysteine
289  <400> SEQUENCE: 32
290  Ser Ala Arg Val Xaa His Gly Pro Ser Val
291  1               5                   10
294  <210> SEQ ID NO: 33
295  <211> LENGTH: 85
296  <212> TYPE: DNA
297  <213> ORGANISM: Synthetic
299  <220> FEATURE:
300  <223> OTHER INFORMATION: M = A or C
302  <220> FEATURE:
303  <223> OTHER INFORMATION: N = A, C, T or G
305  <400> SEQUENCE: 33
306  catgtttcgg ccgattggtg cagacctgca accgamnnmn nmnntcamnn mnnmnnmnna 60
307  gagtgagaat agaaaggtac ccggg                                       85
309  <210> SEQ ID NO: 34
310  <211> LENGTH: 85
311  <212> TYPE: DNA
312  <213> ORGANISM: Synthetic
314  <220> FEATURE:
315  <223> OTHER INFORMATION: M = A or C
317  <220> FEATURE:
318  <223> OTHER INFORMATION: N = A, C, T or G
320  <400> SEQUENCE: 34
321  catgtttcgg ccgattggtg cagacctgca accgamnnmn nmnatcamnn mnnmnnmnna 60
322  gagtgagaat agaaaggtac ccggg                                       85
324  <210> SEQ ID NO: 35
325  <211> LENGTH: 8
326  <212> TYPE: PRT
```

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/937,187

DATE: 02/06/2002
TIME: 18:41:32

Input Set : **A:\Neb-164.app**
Output Set: **N:\CRF3\02062002\I937187.raw**

```
L:11  M:270 C: Current Application Number differs, Replaced Application Number
L:12  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:33  M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:33  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:33  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:252 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:28
L:252 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28
L:252 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:290 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:32
L:290 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:32
L:290 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:306 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:33
L:306 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:33
L:306 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:321 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34
L:321 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:34
L:321 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:383 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:40
L:383 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:40
L:383 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:397 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:41
L:397 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:41
L:397 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
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